10/738454
Search result

Freeform Search

Database: US Pre-Grant Publication Full-Text Database
US Patents Full-Text Database
US OCR Full-Text Database
EPO Abstracts Database
JPO Abstracts Database
Derwent World Patents Index
IBM Technical Disclosure Bulletins

Term: yeast$ near10 surface$ near10 display$ and epitope$ near10 tag$

Display: 100 **Documents in Display Format:** - **Starting with Number** 1

Generate: ○ **Hit List** ◉ **Hit Count** ○ **Side by Side** ○ **Image**

Search | Clear | Interrupt

Search History

DATE: Saturday, July 30, 2005 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=OR			
L47	l8 and agglutinin$	1	L47
L46	agglutinin$ near "a"	50	L46
L45	agglutinin$ near10 subunit$	51	L45
L44	agglutinin$ near10 Aga$	2	L44
L43	agglutinin$ and Aga$	497	L43
L42	agglutinin$ and Agap2 and Aga1p	0	L42
L41	agglutinin$ near10 agap2 and aga1p	0	L41
L40	yeast$ near10 agglutinin$ near10 component$	1	L40
L39	aggultinin$ near10 component$	1	L39
L38	L37 and ferguson and schreuder	1	L38
L37	20040180348	2	L37
L36	l35 and (T near cell$) near10 (binding or receptor$)	105	L36
L35	yeast$ near10 surface$ near10 display$ and epitope$ near10 tag$	146	L35
L34	L8 and anti near3 T near cell	1	L34
L33	L8 and T near cell	2	L33

L32	L8 and T cell	1472912	L32
L31	tagged near5 fus$ near5 protein$ near20 surface$ near10 display$ and yeast	3	L31
L30	tagged near5 fus$ near5 protein$ near20 yeast$ and surface near10 display$	0	L30
L29	yeast$ near29 fusion$ near10 epitope$ near5 tag$ and surface$ near10 display$	14	L29
L28	yeast$ and fusion$ near10 epitope$ near5 tag$ and surface$ near10 display$	498	L28
L27	yeast$ and fusion$ near10 epitope$ and surface$ near10 display$	1266	L27
L26	yeast$ and fusion$ near10 epitope$	7202	L26
L25	L23 and yeast$ near10 (cell$ near5 wall or agglutinin) near10 fus$	6	L25
L24	L23 and yeast$ near10 (cell$ near5 wall or agglutinin) near10 fus$ near10 epitope$	5	L24
L23	direct$ near5 evolution$	2581	L23
L22	yeast$ and cell near5 wall$ near10 epitope$ near5 tag$	6	L22
L21	yeast$ and cell near5 wall$ near10 epitope$	97	L21
L20	L19 and epitope near5 tag$	134	L20
L19	yeast$ near10 surface near10 display$	249	L19
L18	yeast$ near10 cell near10 wall near10 fus$ near10 detect$	0	L18
L17	yeast$ near10 cell near10 wall near10 fus$ near10 epitope$	5	L17
L16	yeast$ near10 cell near10 wall near10 fus$ neare10 epitope$	54858	L16
L15	agglutinin near10 fus$ near10 epitope$	4	L15
L14	agglutinin near10 fus$ near10 epitope$ near5 tag$	0	L14
L13	agglutinin near10 fus$ near10 eptipoe near5 tag$	0	L13
L12	L8 and specificity	1	L12
L11	L8 and avidity	1	L11
L10	L8 and mean$	1	L10
L9	L8 and means	1	L9
L8	20040146976	2	L8
L7	6759243 [pn]	2	L7
L6	6300065 [pn]	2	L6
L5	6423538 [pn]	2	L5
L4	6696251 [pn]	2	L4
L3	6696251	4	L3
L2	6699658 [pn]	2	L2
L1	aga2p	32	L1

END OF SEARCH HISTORY

Refine Search

Your wildcard search against 10000 terms has yielded the results below.
Your result set for the last L# is incomplete.
The probable cause is use of unlimited truncation. Revise your search strategy to use limited truncation.

Search Results -

Terms	Documents
fus$ near10 agglutinin$ near10 T near cell$	0

Database: US Pre-Grant Publication Full-Text Database; US Patents Full-Text Database; US OCR Full-Text Database; EPO Abstracts Database; JPO Abstracts Database; Derwent World Patents Index; IBM Technical Disclosure Bulletins

Search: L11

Refine Search | Recall Text | Clear | Interrupt

Search History

DATE: Friday, July 29, 2005 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=OR			
L11	fus$ near10 agglutinin$ near10 T near cell$	0	L11
L10	agglutinin$ near10 T near cell$ near5 receptor$	0	L10
L9	agglutinin$ near10 T near cell$	20	L9
L8	agglutinin$ near10 epitope near5 tag$	11	L8
L7	agglutinin$ and epitope near5 tag$	254	L7
L6	fusion$ and agglutinin$ and aga2p and aga1p	13	L6
L5	l3 and aga2p	13	L5
L4	fus$ near10 c-termin$ near10 agglutinin	9	L4
L3	c-termin$ near10 agglutinin	29	L3
L2	fusion$ near10 agglutinin near5 aga2p and aga1p	5	L2
L1	fusion$ near10 agglutinin near5 aga2p	10	L1

END OF SEARCH HISTORY

BEGIN 5,6,55,154,155,156,312,399,BIOTECH,BISOCI

```
      Set  Items  Description
      ---  -----  -----------
?

S AGA2P AND FUSION?
             107  AGA2P
         1224583  FUSION?
      S1      80  AGA2P AND FUSION?
?

RD S1
...examined 50 records  (50)
...completed examining records
      S2      25  RD S1 (unique items)
?

S S2 NOT PY>1997
Processing
Processed  10 of  27 files ...
Processing
Processed  20 of  27 files ...
>>>One or more prefixes are unsupported
>>>  or undefined in one or more files.
Completed processing all files
             25  S2
       48791779  PY>1997
      S3       3  S2 NOT PY>1997
?

     Display 3/9/1     (Item 1 from file: 5)
DIALOG(R)File   5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.

0010970143   BIOSIS NO.: 199799604203
 Yeast surface display for screening combinatorial polypeptide libraries
AUTHOR: Boder Eric T; Wittrup K Dane (Reprint)
AUTHOR ADDRESS: Dep. Chem. Eng., Univ. Ill., Urbana, IL 61801, USA**USA
JOURNAL: Nature Biotechnology  15 (6): p553-557 1997 1997
ISSN: 1087-0156
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Display on the yeast cell wall is well suited for engineering
  mammalian cell-surface and secreted proteins (e.g., antibodies,
  receptors, cytokines) that require endoplasmic reticulum-specific
  post-translational processing for efficient folding and activity.
  C-terminal fusion to the Aga2p mating adhesion receptor of Saccharomyces

                                    -more-
?

     Display 3/9/1     (Item 1 from file: 5)
DIALOG(R)File   5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.
  cerevisiae has been used for the selection of scFv antibody fragments
  with threefold decreased antigen dissociation rate from a randomly
  mutated library. A eukaryotic host should alleviate expression biases
  present in bacterially propagated combinatorial libraries. Quantitative
  flow cytometric analysis enables fine discrimination of kinetic
```

parameters for protein binding to soluble ligands.

DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology; Genetics; Immune System--Chemical Coordination and Homeostasis; Metabolism; Methods and Techniques
BIOSYSTEMATIC NAMES: Ascomycetes--Fungi, Plantae; Fungi--Plantae
ORGANISMS: Saccharomyces cerevisiae (Ascomycetes); fungus (Fungi)
COMMON TAXONOMIC TERMS: Fungi; Microorganisms; Nonvascular Plants; Plants
MISCELLANEOUS TERMS: ANALYTICAL METHOD; ANTIBODIES; ANTIBODY ENGINEERING; ANTIGEN; BIOBUSINESS; BIOTECHNOLOGY; CELL WALL; FLOW

-more-

?

Display 3/9/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.
CYTOMETRY; METHODOLOGY; MOLECULAR GENETIC METHOD; MOLECULAR GENETICS; POLYPEPTIDES; PROTEIN ENGINEERING; PROTEINS; RANDOMLY MUTATED LIBRARY; SOLUBLE LIGANDS; YEAST SURFACE DISPLAY
CONCEPT CODES:
02504 Cytology - Plant
03502 Genetics - General
10010 Comparative biochemistry
10052 Biochemistry methods - Nucleic acids, purines and pyrimidines
10054 Biochemistry methods - Proteins, peptides and amino acids
10064 Biochemistry studies - Proteins, peptides and amino acids
10068 Biochemistry studies - Carbohydrates
10506 Biophysics - Molecular properties and macromolecules
13012 Metabolism - Proteins, peptides and amino acids
32000 Microbiological apparatus, methods and media
34502 Immunology - General and methods
BIOSYSTEMATIC CODES:

-more-

?

Display 3/9/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2005 BIOSIS. All rts. reserv.
15100 Ascomycetes
15000 Fungi

- end of record -

?

Display 3/9/2 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2005 Inst for Sci Info. All rts. reserv.

04029309 Genuine Article#: RA331 Number of References: 20
Title: GENETICS OF A-AGGLUTUNIN FUNCTION IN SACCHAROMYCES-CEREVISIAE
Author(s): DENOBEL H; PIKE J; LIPKE PN; KURJAN J
Corporate Source: UNIV VERMONT,COLL MED,DEPT MICROBIOL & MOLEC GENET/BURLINGTON//VT/05405; UNIV VERMONT,COLL MED,DEPT MICROBIOL & MOLEC GENET/BURLINGTON//VT/05405; UNIV VERMONT,COLL AGR & LIFE SCI/BURLINGTON//VT/05405; UNIV VERMONT,VERMONT CANC CTR/BURLINGTON//VT/05405; CUNY HUNTER COLL,DEPT BIOL SCI/NEW YORK//NY/10021; CUNY HUNTER COLL,INST BIOMOLEC STRUCT & FUNCT/NEW

YORK//NY/10021
Journal: MOLECULAR & GENERAL GENETICS, 1995, V247, N4 (MAY 20), P409-415
ISSN: 0026-8925
Language: ENGLISH Document Type: ARTICLE
Geographic Location: USA
Subfile: SciSearch; CC LIFE--Current Contents, Life Sciences

-more-

?

Display 3/9/2 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2005 Inst for Sci Info. All rts. reserv.
Journal Subject Category: GENETICS & HEREDITY; BIOCHEMISTRY & MOLECULAR BIOLOGY
Abstract: The Saccharomyces cerevisiae cell adhesion protein a-agglutinin is composed of an anchorage subunit (Agalp) and an adhesion subunit (Aga2p). Although functional a-agglutinin is expressed only by a cells, previous results indicated that AGA1 RNA is expressed in both a and alpha cells after pheromone induction. Expression of the Aga2p adhesion subunit in alpha cells allowed a-agglutinability, indicating that alpha cells express the a-agglutinin anchorage subunit, although no role for Agalp in alpha cells has been identified. Most of the a-specific agglutination-defective mutants isolated previously were defective in AGA1; a single mutant (La199) was a candidate for an aga2 mutant. Expression of AGA2 under PGK control allowed secretion of active Aga2p from control strains but did not complement the La199 agglutination defect or allow secretion of Aga2p from La199, suggesting that the La199 mutation might identify a new gene required for a-agglutinin

-more-

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Display 3/9/2 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2005 Inst for Sci Info. All rts. reserv.
function. However, the La199 agglutination defect showed tight linkage to aga2::URA3 and did not complement aga2::URA3 in a/a diploids. The aga2 gene cloned from La199 was nonfunctional and contained an ochre mutation. The inability of pPGK-AGA2 to express functional Aga2p in La199 was shown to result from an additional mutation(s) that reduces expression of plasmid-borne genes. AGA2 was mapped to the left arm of chromosome VII approximately 28 cM from the centromere.
Descriptors--Author Keywords: AGGLUTININS ; ADHESION PROTEINS ; YEAST MATING
Identifiers--KeyWords Plus: ALPHA-AGGLUTININ; SEXUAL AGGLUTINATION; SHUTTLE VECTORS; STRUCTURAL GENE; CELL-FUSION; EXPRESSION; PROTEIN
Research Fronts: 93-2330 001 (ACTIN CYTOSKELETAL PROTEINS IN SACCHAROMYCES-CEREVISIAE; SELECTABLE MARKER GENE; ESSENTIAL COMPONENTS)
Cited References:
CAPPELLARO C, 1991, V10, P4081, EMBO J
CHRISTIANSON TW, 1992, V110, P119, GENE

-more-

?

Display 3/9/2 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
(c) 2005 Inst for Sci Info. All rts. reserv.
ECKER DJ, 1987, V262, P3524, J BIOL CHEM

HERSKOWITZ I, 1994, V194, P132, METHOD ENZYMOL
KANG YS, 1990, V10, P2582, MOL CELL BIOL
KURJAN J, 1985, V5, P787, MOL CELL BIOL
LIPKE PN, 1992, V56, P180, MICROBIOL REV
LIPKE PN, 1989, V9, P3155, MOL CELL BIOL
MCCAFFREY G, 1987, V7, P2680, MOL CELL BIOL
RILES L, 1993, V134, P81, GENETICS
ROY A, 1991, V11, P4196, MOL CELL BIOL
SIJMONS PC, 1987, V148, P208, ARCH MICROBIOL
SIKORSKI RS, 1989, V122, P19, GENETICS
TERRANCE K, 1981, V148, P889, J BACTERIOL
TOHOYAMA H, 1982, V186, P322, MOL GEN GENET
TRUEHEART J, 1987, V7, P2316, MOL CELL BIOL
WOJCIECHOWICZ D, 1989, V161, P45, BIOCHEM BIOPH RES CO
WOJCIECHOWICZ D, 1993, V13, P2554, MOL CELL BIOL

-more-

?

Display 3/9/2 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

YANAGISHIMA N, 1984, V17, P403, ENCY PLANT PHYSL N
YANAGISHIMA N, 1976, V17, P439, PLANT CELL PHYSIOL

- end of record -

?

Display 3/9/3 (Item 1 from file: 315)
DIALOG(R)File 315:ChemEng & Biotec Abs

427661 CEABA Accession No.: 28-12-025051 DOCUMENT TYPE: Journal
Title: Yeast surface display for screening combinatorial polypeptide libraries.
AUTHOR: Wittrup, K. D. ; Boder, E. T.
CORPORATE SOURCE: Univ. Illinois Dept. Chem. Eng. Urbana, IL 61801 USA
JOURNAL: Nature Biotechnol., Volume: 15, Issue: 6, Page(s): 553-557
ISSN: 10870156
PUBLICATION DATE: Jun 1997 (970600) LANGUAGE: English
ABSTRACT: Display on the yeast cell wall is suited to engineering mammalian cell-surface and secreted proteins that require endoplasmic reticulum-specific post-translational processing for efficient folding and activity. C-terminal fusion to the Aga2p mating adhesion receptor of Saccharomyces cerevisiae was used for the selection of scFv antibody fragments with 3-fold decreased antigen-dissociation rate from a randomly mutated library. A eukaryotic host should alleviate expression

-more-

?

Display 3/9/3 (Item 1 from file: 315)
DIALOG(R)File 315:ChemEng & Biotec Abs

biases present in bacterially propagated combinatorial libraries.
DESCRIPTORS: English ; protein engineering ; antibodies ; protein folding ; genetic manipulation
SECTION: Genetic Manipulation (53)
DECHEMA CLASSIFICATION: Biology, Microbiology, Molecular Biology
(classification, taxonomy, morphology, physiology, strain improvement,

```
    genetics, ecology, inoculum, maintenance, storage)   (914 );
    Micro-organisms and enzymes: types, physiology, reactions, parasites,
    poisons (143  )

                                - end of record -
?

S AGGLUTININ (5N) FUS?
          110569  AGGLUTININ
         1768658  FUS?
      S4    1161  AGGLUTININ (5N) FUS?
?

S S4 AND YEAST (5N) SURFACE (5N) DISPLAY?
Processed  20 of  27 files ...
Processing
Completed processing all files
            1161  S4
          985635  YEAST
         6854158  SURFACE
         1550429  DISPLAY?
            1010  YEAST(5N)SURFACE(5N)DISPLAY?
      S5      82  S4 AND YEAST (5N) SURFACE (5N) DISPLAY?
?

RD S5
...examined 50 records  (50)
...completed examining records
      S6      21  RD S5 (unique items)
?

S S6 NOT PY>1997
Processing
Processed  10 of  27 files ...
>>>One or more prefixes are unsupported
>>>  or undefined in one or more files.
Completed processing all files
              21  S6
        48791779  PY>1997
      S7      1  S6 NOT PY>1997
?

     Display 7/9/1     (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.
(c) 2005 Thomson Derwent & ISI. All rts. reserv.

0210188  DBR Accession No.: 97-05309
 Construction of a starch-utilizing yeast by cell surface engineering  -
   Saccharomyces cerevisiae strain improvement
AUTHOR: Murai T;  Ueda M;  Yamamura M;  Atomi H;  Shibasaki Y;  Kamasawa N;
     Osumi M; Amachi T; +Tanaka A
CORPORATE AFFILIATE: Univ.Kyoto  Univ.Japan-Women's  Suntory
CORPORATE SOURCE: Department of Synthetic Chemistry and Biological
    Chemistry, Graduate School of Engineering, Kyoto University, Yoshida,
    Sakyo-ku, Kyoto 606-01, Japan.
JOURNAL: Appl.Environ.Microbiol.  (63, 4, 1362-66)  1997
ISSN: 0099-2240  CODEN: AEMIDF
LANGUAGE: English
ABSTRACT:  This  study  reports  on  the  construction  of  a  novel
    starch-utilizing yeast by display of amylolytic enzyme on the cell wall
```

of Saccharomyces cerevisiae. The plasmid pGA11, a multicopy plasmid for

-more-

?

Display 7/9/1 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

expression of the glucoamylase (EC-3.2.1.3)/alpha-agglutinin fusion gene containing the secretion signal peptide sequence of the glucoamylase under the control of the GAPDH promoter, was constructed. The plasmid pGA11 and control plasmid pYE22m were introduced into S. cerevisiae MT8-1. Cells harboring either of the plasmids were inoculated on a plate of modified Burkholder medium containing 2% glucose and 1% soluble starch. The cells harbouring the plasmid pGA11 hydrolyzed the starch. Expression of the fusion protein in S. cerevisiae containing pGA11 was carried out under the control of glyceraldehyde-3-phosphate- dehydrogenase (EC-1.2.1.12) promoter. Glucoamylase activity was detected in the culture medium but in the cell pellet fraction. Results indicated that the glucoamylase was covalently attached to the cell wall. Cell surface engineering is a new way of improving metabolic characteristics of cells. (22 ref)
E.C. NUMBERS: 3.2.1.3; 1.2.1.12
DESCRIPTORS: starch degradation, Saccharomyces cerevisiae strain

-more-

?

Ref	Items	Index-term
E1	1	AU=WITTRUP, K. D
E2	82	AU=WITTRUP, K. D.
E3	97	*AU=WITTRUP, K. DANE
E4	2	AU=WITTRUP, K. P.
E5	16	AU=WITTRUP, K.D.
E6	2	AU=WITTRUP, KARL D
E7	5	AU=WITTRUP, KARL DANE
E8	27	AU=WITTRUP, KD
E9	16	AU=WITTRUP, KD*
E10	5	AU=WITTRUP, KDANE
E11	3	AU=WITTRUP, L
E12	2	AU=WITTRUP, L.

Enter P or PAGE for more

?

Ref	Items	Index-term
E1	1	AU=KRANZ, DAVE M.
E2	12	*AU=KRANZ, DAVID
E3	2	AU=KRANZ, DAVID A
E4	3	AU=KRANZ, DAVID A.
E5	18	AU=KRANZ, DAVID M
E6	116	AU=KRANZ, DAVID M.
E7	1	AU=KRANZ, DAVID R.
E8	2	AU=KRANZ, DELPHINE
E9	19	AU=KRANZ, DIETER
E10	8	AU=KRANZ, DIETMAR
E11	1	AU=KRANZ, DIETMER
E12	62	AU=KRANZ, DM

Enter P or PAGE for more

?

Ref	Items	Index-term
E1	5	AU=KRANZ DANIEL
E2	2	AU=KRANZ DAVE M
E3	3	*AU=KRANZ DAVID
E4	157	AU=KRANZ DAVID M
E5	2	AU=KRANZ DIETER
E6	132	AU=KRANZ DM
E7	1	AU=KRANZ DR
E8	1	AU=KRANZ DS
E9	1	AU=KRANZ DWIGHT S
E10	160	AU=KRANZ E
E11	3	AU=KRANZ E G
E12	4	AU=KRANZ E U

Enter P or PAGE for more

?

Ref	Items	Index-term
E1	1	AU=KIEKE, MATTHEW LANE
E2	6	AU=KIEKE, MC
E3	1	*AU=KIEKE, MICHELE
E4	6	AU=KIEKE, MICHELE C
E5	11	AU=KIEKE, MICHELE C.
E6	1	AU=KIEKE, MICHELE CATHERINE
E7	2	AU=KIEKE, MURRAY
E8	2	AU=KIEKE, MURRAY D
E9	10	AU=KIEKE, MURRAY D.
E10	1	AU=KIEKEBEN D
E11	2	AU=KIEKEBEN, H. H.
E12	1	AU=KIEKEBUSCH B

Enter P or PAGE for more

?

Ref	Items	Index-term
E1	9	AU=KIEKE MC
E2	2	AU=KIEKE MD
E3	2	*AU=KIEKE MICHELE
E4	23	AU=KIEKE MICHELE C
E5	5	AU=KIEKE ML
E6	1	AU=KIEKE MURRAY D
E7	1	AU=KIEKE, B
E8	3	AU=KIEKE, B.
E9	3	AU=KIEKE, D. E.
E10	2	AU=KIEKE, DAGMAR
E11	2	AU=KIEKE, DAN E.
E12	2	AU=KIEKE, DAN EDWARD

Enter P or PAGE for more

?

Ref	Items	Index-term

```
E1          1  AU=BODER, E.T.
E2          1  AU=BODER, ELENA
E3          2 *AU=BODER, ERIC
E4          7  AU=BODER, ERIC T
E5         13  AU=BODER, ERIC T.
E6          1  AU=BODER, ERIC THOMAS
E7          6  AU=BODER, ET
E8          1  AU=BODER, G
E9          9  AU=BODER, G. B.
E10         5  AU=BODER, GB
E11         3  AU=BODER, GEORGE
E12         1  AU=BODER, GEORGE B

          Enter P or PAGE for more
?


Ref    Items  Index-term
E1        14  AU=BODER E.T.
E2         2  AU=BODER ELEK
E3         2 *AU=BODER ERIC
E4        30  AU=BODER ERIC T
E5        17  AU=BODER ET
E6        20  AU=BODER G
E7       171  AU=BODER G B
E8         7  AU=BODER G G
E9         2  AU=BODER G.
E10       44  AU=BODER G.B.
E11        3  AU=BODER G.G.
E12       63  AU=BODER GB

          Enter P or PAGE for more
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